

Exhibit A  
Comparison of the Amino Acid Sequences of  
SEQ ID NO:24 and NP\_660187

FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaGAABJayWj: 1219 aa

>seqid24

vs /tmp/fastaHAACJayWj library

searching /tmp/fastaHAACJayWj library

1344 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 40, opt: 28, gap-pen: -12/ -2, width: 16

Scan time: 0.034

The best scores are:

NP\_660187 ACCESSION:NP\_660187 NID: gi 21729876 re (1344) 4838 opt

>>NP\_660187 ACCESSION:NP\_660187 NID: gi 21729876 ref NP\_ (1344 aa)

initn: 7156 initl: 4838 opt: 4838

Smith-Waterman score: 7274; 85.311% identity in 1382 aa overlap (1-1219:1-1344)

	10	20	30	40	50	60
seqid2	MTRKRTYWVPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP					
	.....					
NP_660	MTRKRTYWVPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP					
	10	20	30	40	50	60
	70	80	90	100	110	120
seqid2	WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL					
	.....					
NP_660	WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
seqid2	SVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLVMLRFQRTLIFDALLGICFCIASVLG					
	.....					
NP_660	SVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLVMLRFQRTLIFDALLGICFCIASVLG					
	130	140	150	160	170	180
	190	200	210	220	230	240
seqid2	PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFQAAVSS					
	.....					
NP_660	PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAAVSS					
	190	200	210	220	230	240
	250	260	270	280	290	300
seqid2	FAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSYFIIG					
	.....					
NP_660	FAFEKLIQFKSVIHITSGEAISFFTGDVNYLFEGVCYGPLVLITCASLVICSISSYFIIG					
	250	260	270	280	290	300
	310	320	330	340	350	360
seqid2	YTAFAIAILCYLLVFPLEVFMTMAVKAQHHTSEVSDQRIRVTSEVLTCIKLIKMYTWEKP					

NP_660	YTA	FIA	ILCY	LLVF	PLAV	FMT	RM	AVKA	QHHT	SEV	SDQ	RIR	VT	SEV	LT	CI	KL	IK	MY	TW	EK	P	
	310				320				330				340				350				360		
				370			380			390			400				410				420		
seqid2	F	A	K	I	E	D	L	R	R	K	E	R	K	L	L	E	K	C	G	L	V	Q	
	.....																						
NP_660	F	A	K	I	E	D	L	R	R	K	E	R	K	L	L	E	K	C	G	L	V	Q	
	370				380				390				400				410				420		
				430			440			450			460				470				480		
seqid2	L	A	S	L	N	L	L	R	L	S	V	F	F	V	P	I	A	V	K	G	L	T	
	.....																						
NP_660	L	A	S	L	N	L	L	R	L	S	V	F	F	V	P	I	A	V	K	G	L	T	
	430				440				450				460				470				480		
				490			500			510			520				530				540		
seqid2	L	S	W	Q	Q	T	C	P	G	I	V	N	G	A	L	E	L	E	R	N	G	H	
	.....																						
NP_660	L	S	W	Q	Q	T	C	P	G	I	V	N	G	A	L	E	L	E	R	N	G	H	
	490				500				510				520				530				540		
				550			560			570			580				590				600		
seqid2	G	V	C	G	N	T	G	S	G	K	S	S	L	S	A	I	L	E	E	M	H	L	
	.....																						
NP_660	G	V	C	G	N	T	G	S	G	K	S	S	L	S	A	I	L	E	E	M	H	L	
	550				560				570				580				590				600		
				610			620			630			640				650				660		
seqid2	A	R	Y	L	Q	V	L	H	C	C	S	L	N	R	D	L	E	L	L	P	F	G	
	.....																						
NP_660	A	R	Y	L	Q	V	L	H	C	C	S	L	N	R	D	L	E	L	L	P	F	G	
	610				620				630				640				650				660		
				670			680			690			700				710				720		
seqid2	L	S	A	V	D	A	H	V	G	K	H	I	F	E	E	C	I	K	K	T	L	R	
	.....																						
NP_660	L	S	A	V	D	A	H	V	G	K	H	I	F	E	E	C	I	K	K	T	L	R	
	670				680				690				700				710				720		
				730			-----																
seqid2	Q	K	K	G	K	Y	A	Q	L	I	Q	K	M	H	K	E	A	T	S	D	M	L	
	.....																						
NP_660	Q	K	K	G	K	Y	A	Q	L	I	Q	K	M	H	K	E	A	T	S	D	M	L	
	730				740				750				760				770				780		
				-----																			
seqid2	-----																						
NP_660	E	E	M	E	E	G	S	L	S	W	R	V	Y	H	H	Y	I	Q	A	A	G	G	
	790				800				810														

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NP_660 NKVFRCPMSFFDTIPIGRLLNCFAGDLEQLDQLLPIFSEQFLVLSLMVIAVLLIVSVLSP
      910      920      930      940      950      960

      800      810      820      830      840      850
seqid2 YILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPFLFSHILNSLQGLSSIHVYGKTED
      .....
NP_660 YILLMGAIIMVICFIYYMMFKKAIGVFKRLENYSRSPFLFSHILNSLQGLSSIHVYGKTED
      970      980      990     1000     1010     1020

      860      870      880      890      900      910
seqid2 FISQFKRLTDAQNNYLLLFSSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMA
      .....
NP_660 FISQFKRLTDAQNNYLLLFSSSTRWMALRLEIMTNLVTLAVALFVAFGISSTPYSFKVMA
      1030     1040     1050     1060     1070     1080

      920      930      940      950      960      970
seqid2 VNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGE
      .....
NP_660 VNIVLQLASSFQATARIGLETEAQFTAVERILQYMKMCVSEAPLHMEGTSCPQGWPQHGE
      1090     1100     1110     1120     1130     1140

      980      990     1000     1010     1020     1030
seqid2 IIFQDYHMKYRDNTPTVLHGINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRIL
      .....
NP_660 IIFQDYHMKYRDNTPTVLHGINLTIRGHEVVGIVGRTGSGKSSLGMALFRLVEPMAGRIL
      1150     1160     1170     1180     1190     1200

      1040     1050     1060     1070     1080     1090
seqid2 IDGVDICSIGLEDLRSKLSVIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKEI
      .....
NP_660 IDGVDICSIGLEDLRSKLSVIPQDPVLLSGTIRFNLDPFDRHTDQQIWDALERTFLTKEI
      1210     1220     1230     1240     1250     1260

      1100     1110     1120     1130     1140     1150
seqid2 SKFPKKLHTDVVENGGNFSVGERQLLCIARAVLRNSKIILIDEATASIDMETDTLIQRTI
      .....
NP_660 -----ILIDEATASIDMETDTLIQRTI
      1270     1280

      1160     1170     1180     1190     1200     1210
seqid2 REAFQGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSS
      .....
NP_660 REAFQGCTVLVIAHRVTTVLNCDHILVMGNGKVVEFDRPEVLRKKPGSLFAALMATATSS
      1290     1300     1310     1320     1330     1340

seqid2 LR
      ::
NP_660 LR

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